



(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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Msearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

on: Thu Aug 21 10:07:45 1997; Msearch time 876.69 Seconds

Tabular output not generated. 894.092 Million cell updates/sec

Title: >US-08-469-637A-1
(1-1527) from US08469637A.seq
Description: 1527 1 CGCCGACGCCGCCGCTCCAA.....TTCAGCTGAGAAAAA 1527
Perfect Score: 1527
N.A. Sequence: GCGGCGCGCGCGCGAGGTTT.....AAGTTGACCTTTT
Comp: GCGGCGCGCGCGCGAGGTTT.....AAGTTGACCTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 707517 seqs, 256659390 bases x 2

Post-processing: Minimum Match 0
Listing first 45 summaries

Database:

EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99

Database:

EST-STS-TMO

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165:EST165 166:EST166 167:EST167 168:EST168 169:EST169
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

Statistics: Mean 11.463; Variance 1.911; scale 5.997

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	563	36.9	602	195	AA037313	zc52h03.r1 Soares sen 0.00e+00
2	327	21.4	346	73	H88769	YW23512.r1 Homo sapie 0.00e+00
3	187	12.2	458	49	HUM366H09B	Human aorta CDNA 5'-e 0.00e+00
4	173	11.3	370	49	HUM345E08B	Human aorta CDNA 5'-e 0.00e+00
5	114	7.5	303	49	HUM365F01B	Human aorta CDNA 5'-e 2.56e-195
6	114	7.5	387	49	HUM365H11B	Human aorta CDNA 5'-e 2.56e-195
7	56	3.7	157	140	C02463	HUMG50012349, Human G 4.02e-65
8	24	1.6	504	5	T72414	YC72407.r1 Homo sapie 1.55e-06
9	23	1.5	344	61	H14106	YM26805.r1 Homo sapie 3.63e-05
10	23	1.5	442	5	T71938	YE07604.r1 Homo sapie 3.63e-05
11	23	1.5	470	2	T60480	YB95403.r1 Homo sapie 3.63e-05
12	21	1.4	232	53	R94906	YG39B08.r1 Homo sapie 1.36e-02
13	22	1.4	221	44	H37487	15616 Arabidopsis th 7.51e-04
14	22	1.4	253	129	H5C08E062	H. sapiens partial CD 1.36e-02
15	22	1.4	267	148	W10583	ma3f10.r1 Soares mou 7.51e-04
16	22	1.4	300	183	AA100384	zn46h08.r1 Stratiogene 7.51e-04
17	22	1.4	301	48	HUM245F10B	Human aorta CDNA 5'-e 7.51e-04
18	21	1.4	325	65	H29337	YM60807.r1 Homo sapie 1.36e-02
19	21	1.4	325	112	ATRS3517	A. thaliana transcrib 1.36e-02
20	21	1.4	325	19	T54964	YD42403.r1 Homo sapie 1.36e-02
21	22	1.4	330	13	R1CC0437A	Rice CDNA, partial se 7.51e-04
22	22	1.4	339	88	H65000	YU66410.r1 Homo sapie 1.36e-02
23	22	1.4	360	164	C14856	Human fetal brain CDN 7.51e-04
24	21	1.4	362	5	T70903	YC49803.r1 Homo sapie 1.36e-02
25	21	1.4	380	187	AA142584	mq64e05.r1 Soares 2ND 1.36e-02
26	21	1.4	385	180	AA087288	mol1d06.r1 Life Tech 7.51e-04
27	22	1.4	387	109	HSDH23G03	H. sapiens partial CD 7.51e-04
28	21	1.4	395	5	T71079	YC50C04.r1 Homo sapie 1.36e-02
29	22	1.4	406	126	W76826	me79g11.r1 Soares mou 7.51e-04
30	21	1.4	408	41	R27233	YH33801.r1 Soares mou 1.36e-02
31	22	1.4	410	6	T74804	YC60004.r1 Homo sapie 7.51e-04
32	21	1.4	447	184	AA011021	ze34c01.s1 Soares ret 1.36e-02
33	21	1.4	450	131	N68886	TG5E4Tzy39d10.r1 Toxop 1.36e-02
34	21	1.4	453	193	AA164719	zo39f04.s1 Stratiogene 1.36e-02
35	22	1.4	453	111	N21157	YX47d01.r1 Homo sapie 7.51e-04
36	21	1.4	465	193	AA164056	mt67g06.r1 Soares mou 1.36e-02
37	22	1.4	465	5	T77351	YD72410.r1 Homo sapie 7.51e-04
38	22	1.4	472	57	T42477	5740 Arabidopsis thal 7.51e-04
39	21	1.4	472	147	AA003244	mq46g01.r1 Soares mou 1.36e-02
40	21	1.4	478	172	AA061066	mj96h11.r1 Soares mou 1.36e-02
41	21	1.4	480	175	W81931	me93c11.r1 Soares mou 1.36e-02
42	22	1.4	493	55	R1CS1559A	Rice CDNA, partial se 7.51e-04
43	21	1.4	500	94	N38845	YH80411.s1 Homo sapie 1.36e-02
44	21	1.4	766	117	W28026	55c10 Human retina CD 7.51e-04
45	21	1.4	798	115	W22001	6268 Human retina CDN 1.36e-02

ALIGNMENTS

RESULT 1
LOCUS AA037313 602 bp mRNA EST 25-NOV-1996
DEFINITION zc52h03.r1 Soares senescent fibroblasts NBHSF Homo sapiens CDNA
ACCESSION AA037313
NID G1512420
KEYWORDS EST.

REFERENCE	ORGANISM	SOURCE	TITLE	COMMENT
1 (bases 1 to 602)	human.	human.		
1	Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata; Vertebrata: Euthera; Primates; Catarrhini; Hominiidae; Homo.			
1	Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M., Holman, M., Hiltman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.			
			The Mashu-Merck EST Project	
			Unpublished (1995)	
			Contact: Wilson RK	
			Mashu-Merck EST Project	
			Washington University School of Medicine	
			4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
			Tel: 314 286 1800	
			Fax: 314 286 1810	
			Email: est@wustl.wustl.edu	
			This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	
			Insert Length: 1203 Std Error: 0.00	
			Seq primer: -28M13 rev2 from AmerSham	
			High quality sequence stop: 435.	
			Location/Qualifiers	
			1..602	
			/organism="Homo sapiens"	
			/note="vector: p713D (Pharmacia) with a modified polylinker V-type; phagemid; site 1: Not I; site 2: Eco RI; TGTACCATTCGATCGAGGAGGCGGCGATTTTTTTTTTTT 3' double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p713 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Benton Soares and M. Fatima Ronaldo."	
			/clone="325973"	
			/clone_lib="Soares senescent fibroblasts NDHS"	
			/tissue_type="senescent fibroblast"	
			/lab_host="DH10B (ampicillin resistant)"	
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			<1...>602	
			209 a. 128 c 136 g 126 t 3 others	
			BASE COUNT	
			ORIGIN	
			Query Match 36.9%; Score 563; DB 195; Length 602;	
			Best Local Similarity 98.7%; P-adj: 0.00e+00;	
			atches 588; Conservative 0; Mismatches 4; Indels 4; Gaps 4;	
			2 tcttaagaccctctagaacaacacacaattcgcgaagctcttgcctctgtaactca 61	
			2y TCTTAAGACCCCTGTAGAAACACACAAATT -GCGAGTCTTGGTCTCTGCTAACTCA 569	
			62 gaaaggaatgcaacacacacacacacatagtgccggaacagtgaaatcaactcaaaatg 121	
			2y GAAAGGAATGCAACACACACACACATATGTCCGGAACAGTGAATCAACTCAAAATG 629	
			122 tggaaatagatgtttacccctgtgtgtggaggatcttctcaagttgttccttacaagt 181	
			2y TGGAAATAGATGTTTACCCCTGTGTGGAGGCGATTCTTCAAGTTGCTTCTTCAAAAGTT 669	
			182 taagcctaaccgagcttagtgtcttggtagaacaatttgcctggcacaagttaacgcaga 241	
			2y TACGCCTAACGCGCTTAGTGTCTTGGTAGAACAATTTCCTGGCACCAATAAAGCAGA 749	
			242 gaggtgtagagagataaagcggcaacacagctcacaagaacagagacttccagctgtgaa 301	
			2y GAGGTGTAGAGAGATAAAGCGCAACACAGCTCACAAGAACACAGACTTCCAGGTGTGAA 809	
			302 gttatggaaacatcaaaacaaagccaagatattgttaagaagaatctcaagatatgtga 361	
			2y GTTATGGAAACATCAAAACCAAGCCAAAGATATTGTCAAGAAGATCTCCAAAGATATTGA 869	

LOCUS	2	H88769	346 bp	mrna	EST	22-NOV-1995
DEFINITION		Y239312.1	Homo sapiens	CDNA	253126 5'	
ACCESSION		H88769				
NID		91071029				
KEYWORDS		EST.				
SOURCE		human clone=253126 primer=M13RPI library=Morton Fetal Cochlea vector=PBLuescript SK ⁺ host=SOLR cells (Xenamycin resistant) Rsite=EcORI Rsite2=XhoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcORI adaptors were ligated to the blunt ends. adaptor linker: GAATTGGCAGCGAG.				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homindae; Homo.				
REFERENCE		1 (Phases 1 to 346)				
AUTHORS		Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maier,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Treaskis,E., Westerton,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE		WashU-Merck EST Project				
JOURNAL		Unpublished (1995)				
COMMENT		Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 278 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Source 1..346 /organism="Homo sapiens" /clone="253126" <1..>346				
MRNA		104 a	71 c	62 g	106 t	3 others
BASE COUNT						
ORIGIN						
Query Match		21.4%	Score 327;	DB 73;	Length 346;	
Best Local Similarity		98.3%;	Pred. No. 0.00e+00;			
Matches		340;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 2;
Db	1	tcagggtccttcacagcttcacaaatgtaacatgtaacaggaagtattttggaatacga	60			
QY	1151	TCAGGTCCTTCACAGCTTCACAAATGTATCATGAGAGTATTTTGAATGA	1210			
Db	61	taggtaacccggtcccaatcgtaanaataagctgcttataacacggaatggccatggac	120			
QY	1211	TAGGTAAACCGGTCCATCGTAAATAAGCTGCTTATTAACGTGAATAATGGCCATTGAGC	1270			

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Db 121 ttttctcncaatgtggcagatcccatgagtgaactgtttctcagcacttgagg 180
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Qy 1271 TGTTCCTCCACAAATGGGAGATCCCATGATGAGTAACATGTTCTCAGCACTTGAGG 1330
      |||||||
Db 181 ctccagatgatactttctcattcccaatgactaattttgcacagggtaactaaagaa 240
      |||||||
Qy 1331 CTTTCAGTGAATCTTTCTCTACTTACCACTGACTAATTTTGCACAAAGGCTACTAAAGAAA 1390
      |||||||
Db 241 ctatgagtgtgagaagagactaacatctcctcccaataaaccaccaatggttaactcaac 300
      |||||||
Qy 1391 CTATGATGTGAGAAAGAGACTACATCTCTCCCAATAAACCCCAATGCTT-AAATCCAAC 1449
      |||||||
Db 301 tttcagatctgagatcgttattctactgtgactatntttccctntta 346
      |||||||
Qy 1450 TGTGAGATCTGGATCGTTATCTACTG-ACATATTATTTCCCTTATTA 1494
      |||||||

PSSULT 3 HUM366H09B 458 bp mRNA EST 29-AUG-1995
INITIATION Human aorta cDNA 5'-end GEN-366H09.
ACCESSION D63125
NID 9968050
KEYWORDS EST(expressed sequence tag); Human aorta; similar to none(May 29,1995)
SOURCE Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
          cDNA to mRNA.
ORGANISM Homo sapiens
          Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
          Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
          Takachi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y.,
          Maekawa,H., Shin,S. and Nakamura,Y.
          Unpublished(303)
JOURNAL Submitted (30-May-1995) to DDBJ by:
          Tsutomu Fujiwara
          Otsuka GEN Research Institute
          Otsuka Pharmaceutical Co.,Ltd
          463-10 Kagasuno Kawauchi-cho
          Tokushima, Tokushima
          771-01
          Japan
          Phone: 0886-65-2888
          Fax : 0886-37-1035.
          Location/Qualifiers
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          source
          1..458
          /organism="Homo sapiens"
          /clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
BASE COUNT 157 a 74 c 66 g 161 t
ORIGIN
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Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
LOCUS HUM345E08B 370 bp mRNA EST 29-AUG-1995
DEFINITION Human aorta cDNA 5'-end GEN-345E08.
ACCESSION D62967
NID 9966741
KEYWORDS EST(expressed sequence tag); Human aorta; similar to none(May 29,1995)
SOURCE Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
          cDNA to mRNA.
ORGANISM Homo sapiens
          Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 370)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
          Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
          Takachi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y.,
          Maekawa,H., Shin,S. and Nakamura,Y.
          Unpublished(303)
JOURNAL Submitted (30-May-1995) to DDBJ by:
          Tsutomu Fujiwara
          Otsuka GEN Research Institute
          Otsuka Pharmaceutical Co.,Ltd
          463-10 Kagasuno Kawauchi-cho
          Tokushima, Tokushima
          771-01
          Japan
          Phone: 0886-65-2888
          Fax : 0886-37-1035.
          Location/Qualifiers
FEATURES
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          /clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
BASE COUNT 122 a 63 c 55 g 127 t
ORIGIN
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Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 187; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Query Match 1.4% Score 22; DB 148; Length 267;
 Best Local Similarity 75.0%; Pred. No. 7.51e-04;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

b 31 gaagctgctggaagcgagagagcatgattctctgctctgc 74
 |||||
 3p 931 GAAGCTGCTCGAAGCTGAGGTAGCATGTCCAAATGCGCGCTGC 888

Search completed: Thu Aug 21 10:35:06 1997
 Job time : 1641 secs.